

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Collins, Mary
Donaldson, Debra
Fitz, Lori
Neben, Tamlyn
Whitters, Matthew
Wood, Clive

(ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
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(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.
(B) REGISTRATION NUMBER: 32,724
(C) REFERENCE/DOCKET NUMBER: GI5268

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 256..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCTGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA AGATTGCTTG	60
CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTG CTTCACGTA TAAGGAAGGA	120
AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG GTCTTGTGAT	180
AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA	240
CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile	291
1 5 10	
CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro	339
15 20 25	
CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr	387
30 35 40	
TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr	435
45 50 55 60	
CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys	483
65 70 75	
ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn	531
80 85 90	
AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr	579
95 100 105	
AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile	627
110 115 120	
TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile	675
125 130 135 140	
TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA	723

Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Lys	Thr	
			145			150					155					
GTA	TAT	TCT	GAT	ACC	AAC	TAT	ACC	ATG	TTT	TTC	TGG	TAT	GAG	GGC	TTG	771
Val	Tyr	Ser	Asp	Thr	Asn	Tyr	Thr	Met	Phe	Phe	Trp	Tyr	Glu	Gly	Leu	
	160					165						170				
GAT	CAT	GCC	TTA	CAG	TGT	GCT	GAT	TAC	CTC	CAG	CAT	GAT	GAA	AAA	AAT	819
Asp	His	Ala	Leu	Gln	Cys	Ala	Asp	Tyr	Leu	Gln	His	Asp	Glu	Lys	Asn	
	175					180					185					
GTT	GGA	TGC	AAA	CTG	TCC	AAC	TTG	GAC	TCA	TCA	GAC	TAT	AAA	GAT	TTT	867
Val	Gly	Cys	Lys	Leu	Ser	Asn	Leu	Asp	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	
	190				195					200						
TTT	ATC	TGT	GTT	AAT	GGA	TCT	TCA	AAG	TTG	GAA	CCC	ATC	AGA	TCC	AGC	915
Phe	Ile	Cys	Val	Asn	Gly	Ser	Ser	Lys	Leu	Glu	Pro	Ile	Arg	Ser	Ser	
	205			210			215			220						
TAT	ACA	GTT	TTT	CAA	CTT	CAA	AAT	ATA	GTT	AAA	CCA	TTG	CCA	CCA	GAA	963
Tyr	Thr	Val	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Leu	Pro	Pro	Glu	
	225				230			235								
TTC	CTT	CAT	ATT	A	GTG	GAG	AAT	TCC	ATT	GAT	ATT	AGA	ATG	AAA	TGG	1011
Phe	Leu	His	Ile	Ser	Val	Glu	Asn	Ser	Ile	Asp	Ile	Arg	Met	Lys	Trp	
	240			245			250									
AGC	ACA	CCT	GGA	GGA	CCC	ATT	CCA	CCA	AGG	TGT	TAC	ACT	TAT	GAA	ATT	1059
Ser	Thr	Pro	Gly	Gly	Pro	Ile	Pro	Pro	Arg	Cys	Tyr	Thr	Tyr	Glu	Ile	
	255				260			265								
GTG	ATC	CGA	GAA	GAC	GAT	ATT	TCC	TGG	GAG	TCT	GCC	ACA	GAC	AAA	AAC	1107
Val	Ile	Arg	Glu	Asp	Asp	Ile	Ser	Trp	Glu	Ser	Ala	Thr	Asp	Lys	Asn	
	270			275			280									
GAT	ATG	AAG	TTG	AAG	AGG	AGA	GCA	AAT	GAA	AGT	GAA	GAC	CTA	TGC	TTT	1155
Asp	Met	Lys	Leu	Lys	Arg	Arg	Ala	Asn	Glu	Ser	Glu	Asp	Leu	Cys	Phe	
	285			290			295			300						
TTT	GTA	AGA	TGT	AAG	GTC	AAT	ATA	TAT	TGT	GCA	GAT	GAT	GGA	ATT	TGG	1203
Phe	Val	Arg	Cys	Lys	Val	Asn	Ile	Tyr	Cys	Ala	Asp	Asp	Gly	Ile	Trp	
	305				310			315								
AGC	GAA	TGG	AGT	GAA	GAG	GAA	TGT	TGG	GAA	GGT	TAC	ACA	GGG	CCA	GAC	1251
Ser	Glu	Trp	Ser	Glu	Glu	Cys	Trp	Glu	Gly	Tyr	Thr	Gly	Pro	Asp		
	320			325			330									
TCA	AAG	ATT	ATT	TTC	ATA	GTA	CCA	GTT	TGT	CTT	TTC	TTT	ATA	TTC	CTT	1299
Ser	Lys	Ile	Ile	Phe	Ile	Val	Pro	Val	Cys	Leu	Phe	Phe	Ile	Phe	Leu	
	335				340			345								
TTG	TTA	CTT	CTT	TGC	CTT	ATT	GTG	GAG	AAG	GAA	GAA	CCT	GAA	CCC	ACA	1347
Leu	Leu	Leu	Leu	Cys	Leu	Ile	Val	Glu	Lys	Glu	Glu	Pro	Glu	Pro	Thr	
	350			355			360									

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID N

Met	Ala	Phe	Val	His	Ile	Arg	Cys	Leu	Cys	Phe	Ile	Leu	Leu	Cys	Thr
1					5					10					15
Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe															
					20					25					30
Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys															
					35					40					45
Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu															
					50					55					60
Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr															
					65					70					75
															80
Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu															
					85					90					95
Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu															
					100					105					110
Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly															
					115					120					125
Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp															
					130					135					140
Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp															
					145					150					160
Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu															

165 170 175

Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys
 180 185 190

Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val
 195 200 205

Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe
 210 215 220

Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile
 225 230 235 240

Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly
 245 250 255

Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu
 260 265 270

Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu
 275 280 285

Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys
 290 295 300

Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser
 305 310 315 320

Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile
 325 330 335

Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu
 340 345 350

Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His
 355 360 365

Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys
 370 375 380

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 103..1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC 60
GGCGGGGAGA GAGGCAATAT CAAGGTTTA AATCTCGGAG AA ATG GCT TTC GTT 114
Met Ala Phe Val
1
TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT 162
Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
5 10 15 20
GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG 210
Gly Cys Thr Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
25 30 35
GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA 258
Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
40 45 50
TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA 306
Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
55 60 65
TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC 354
Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
70 75 80
ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC 402
Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
85 90 95 100
ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA 450
Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
105 110 115
TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA 498
Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro
120 125 130
CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC 546
Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr
135 140 145
AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT 594
Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu
150 155 160
CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT 642
Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
165 170 175 180

265 266 267 268 269

GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly 185 190 195	690
TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile 200 205 210	738
TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe 215 220 225	786
ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu 230 235 240	834
ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC ATA Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile 245 250 255 260	882
CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG ATC Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile 265 270 275	930
AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA ACA Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr 280 285 290	978
TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA GTA Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val 295 300 305	1026
AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT GAG Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu 310 315 320	1074
TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA ACT Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr 325 330 335 340	1122
TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT ATA Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile 345 350 355	1170
TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA ATG Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met 360 365 370	1218
ATT CCA GAA TTT TTC TGT GAT ACA TGA AGACTTCCA TATCAAGAGA Ile Pro Glu Phe Phe Cys Asp Thr *	1265
375 380	
CATGGTATTG ACTAACAGT TTCCAGTCAT GGCAAATGT TCAATATGAG TCTCAATAAA	1325
CTGAATTTT CTTGCGAAAAA AAAAAAAAAAA AAATCCGCGG ATCC	1369

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro

225	230	235	240
Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu			
245	250		255
Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr			
260	265		270
Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val			
275	280		285
Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu			
290	295		300
Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly			
305	310	315	320
Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu			
325		330	335
Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu			
340	345		350
Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr			
355	360		365
Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr *			
370	375		380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

KSRCTCCABK CRCTCCA

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAGTTAAC CATTGCCACC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCCATTCGC TCCAAATTCC

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTCTATCTT ACTTTTACTC G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCTGAGCA ATAAATATTC AC

22